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Conference Abstract

The ASV Portal Allows for Efficient Handling of DNA Derived Data in the Living Atlas

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Abstract

The Living Atlas platform functions as the national hub for integration of biodiversity data with environmental and contextual information in many countries, but it has had limited functionality for species occurrence data derived from DNA sequences. Meanwhile, molecular methods for species observation, such as metabarcoding of environmental DNA, are becoming increasingly important for documenting the diversity of life. To incorporate this rapidly growing data source into the platform, we developed the Amplicon Sequence Variant (ASV) portal: a web interface for DNA sequence-derived observations in the Living Atlas.

We identified three key features that would enhance the utility of the atlas platform for species occurrence data derived from metabarcoding: 1) storage of the processed barcode sequences (ASVs) underlying such occurrences, along with the ability to locate them using sequence alignment search; 2) the option to search for data based on sequencing details, such as target genes and primers; and 3) the possibility to update the taxonomic annotation of observed ASVs as reference databases evolve.

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In this presentation, we demonstrate how these features have been implemented in the ASV portal, which now operates as a module within the Swedish Biodiversity Data Infrastructure (SBDI). We provide a brief overview of the underlying architecture and its integration with the Living Atlas and Global Biodiversity Information Facility (GBIF) platforms, showcase the online functionality, and conclude by discussing challenges and future development plans.

Keywords

biodiversity informatics, species occurrence, Darwin Core standard, amplicon sequencing, metabarcoding, eDNA, BLAST

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Conflicts of interest

The authors have declared that no competing interests exist.